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OM protein - protein search, using SW model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)
420.957 Million cell updates/sec

Title: US-08-325-278B-1_COPY_81_152

Perfect score: 371

Sequence: 1 KETPTEPKVEYTIKANLY.....GEYTVIDVADKGTYTLNIRKFG 72

Scoring table: BLOSUM62

Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters:

830525

DB seq length: 0

Max DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL;23:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mbuc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1

053291 PRELIMINARY; PRT: 455 AA.

ID Q53291; AC Q53291;

DT 01-NOV-1996 (TREMBLrel. 01; Created)

DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19; Last annotation update)

DE Protein LG (Fragment).

OS Streptococcus sp.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TAXID=1306;

RN [1]

RP SEQUENCE FROM N.A.; PubMed=1460053;

RX MEDLINE=93094233; PubMed=1460053;

RA Kihlberg B.M., Sjobring U., Kastren W., Björck L.;

RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties."

RL J. Biol. Chem. 267:25583-25588(1992).

DR EMBL: S5009; AAA03280; 1..

DR HSSP: P06554; 1PGX

DR InterPro; IPR003147; B1.

DR InterPro; IPR00724; Igg_bind_B.

DR Pfam: PF02246; B1; 4.

DR Pfam: PF01378; Igg_binding_B; 2.

FT NON_TER 455_455

SQ SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64:

Query Match 100.0% Score 371; DB 2; Length 455;

Best Local Similarity 100.0% Pred No. 4.7e-29; Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKVEYTIKANLYIADGKTQTAEYRADAALKDNGEYTVDVA 60

|||||||||||||||||||||||||||||||||||||||||||||||||||

Db 102 KEKTPPEPKVEYTIKANLYIADGKTQTAEYRADAALKDNGEYTVDVA 161

Qy 61 DKGYTNIKPG 72

|||||||||||||||||||||||||||||||||||||||||||

Db 162 DKGYTNIKPG 173

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	371	100.0	455	2	Q53291	
2	371	100.0	719	2	Q51912	051912 peptostrept
3	308	83.0	992	2	Q51918	051918 peptostrept
4	98.5	26.5	216	4	Q9BPV7	Q9bpv7 homo sapien
5	98.5	26.5	398	4	Q9BPV1	Q9bpv1 homo sapien
6	93.5	25.2	398	11	Q9CZ02	Q9CZ02 mus musculus
7	93.5	25.2	398	11	Q91WD1	Q91wd1 mus musculus
8	89.5	24.1	1576	16	Q8ZEY8	Q8zev8 yersinia pestis
9	73	19.7	588	2	Q9S0T6	Q9s0t6 escherichia
10	70	18.9	1498	2	Q8IDP2	Q8idp2 plasmodium
11	69.5	18.7	256	5	Q27039	Q27039 theileria
12	69.5	18.7	256	5	Q27029	Q27029 theileria
13	69.5	18.7	279	2	Q9ADY8	Q9ad08 ehrlichia
14	69.5	18.7	280	5	Q27030	Q27030 theileria
15	69.5	18.7	451	2	Q9Z4J9	Q9z4j9 lactobacilli
16	69.5	18.7	623	2	Q9F4L0	Q9f4l0 fibrobacter

RESULT 2

RP SEQUENCE FROM N.A.

Q51912 PRELIMINARY; PRT; 719 AA.

ID 051912; STRAIN=316;

AC RX MEDLINE=95078460; PubMed=7987012;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE Peptidoglycan precursor.

OS Peptostreptococcus magnus.

OC Bacteria; Firmicutes; Clostridia; Clostridiales;

OC Peptostreptococaceae; Finegoldia.

OX NCBI_TaxID=1260;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=112;

RX MEDLINE=90215984; PubMed=2108927;

Kasten W., Holst E., Nielsen E., Sjöbring U., Björck L.; "Protein L, a bacterial immunoglobulin-binding protein and possible virulence determinant"; Infect. Immun. 58:1217-1222(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=312;

RX MEDLINE=92316971; PubMed=1618782;

RA Björck L., Sjöbring U., Kasten W.; Structure of peptostreptococcal protein L and identification of repeated immunoglobulin light chain-binding domain.;" J. Biol. Chem. 267:12820-12825(1992).

CC -1. SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).

DR EMBL: M86697; ARX:25612.1; -.

DR InterPro; IPR004829; Csurface_antigen.

DR InterPro; IPR004899; Gram_pos_anchor.

DR InterPro; IPR006192; LPXTG.

DR Pfam; PF02246; BL; 5.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR Prodrom; PD153432; Csurface_antigen; 1.

DR TIGRFAM; TIGR01167; LPXTG anchor; 1.

DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.

KW Cell wall; Peptidoglycan-anchor; Signal.

FT SIGNAL 1 18 POTENTIAL.

CHAIN 19 719 PROTEIN L.

SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100 0%; Score 371; DB 2; Length 719;

Best Local Similarity 100.0%; Pred. No. 8.1e-29; Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEEVTKANLIYADGKTOTAEFKGTFEEATAEAYRADALKNDNGEYTVDA 60

Db 174 KEKTPPEEVTKANLIYADGKTOTAEFKGTFEEATAEAYRADALKNDNGEYTVDA 233

Qy 61 DKGTYNIKFG 72

Db 234 DKGTYNIKFG 245

RESULT 3

RP SEQUENCE FROM N.A.

Q51918 PRELIMINARY; PRT; 992 AA.

ID 051918; STRAIN=316;

AC RX MEDLINE=95078460; PubMed=7987012;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE Protein L precursor.

OS Peptostreptococcus magnus.

OC Bacteria; Firmicutes; Clostridia; Clostridiales;

OC Peptostreptococaceae; Finegoldia.

OX NCBI_TaxID=1260;

RESULT 4

RP Q9BPV7 PRELIMINARY; PRT; 216 AA.

ID Q9BPV7; PRELIMINARY; PRT; 216 AA.

AC Q9BPV7; PRELIMINARY; PRT; 216 AA.

DR DT 01-JUN-2001 (TREMBLrel. 17, Created)

DR DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DR DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DR DE Similar to BN51 (BHR21) temperature sensitivity complementing.

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBITaxonID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.

DR Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003039; AAH030391; -

DR EMBL; BC000516; AAH005161; -

SQ SEQUENCE 216 AA; 24806 MW; F39028AECAADB04 CRC64;

Query Match 26 5%; Score 98.5; DB 4; Length 216;

Best Local Similarity 34.6%; Pred. No. 0.0e+0; Matches 28; Conservative 10; Mismatches 24; Indels 19; Gaps 3;

Qy 3 KTPPEEVTKANLIYADGKTOTAEFKGTFEEATAEAYRADALKNDNGEYDAKK 50

Db 66 KKEPKEEVTKKEKRERDRDREGHGRGRRGAPEVIOSHSTFEQGPAAEMK----KK 120

Qy 51 DNGTYTVADKG--YTLNK 69

Db 121 GNWWRTRVDVSDMGPSHIINJK 141

RESULT 5

Q9BPZ1

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
(without alignments)

Title: US-08-325-278B-1_COPY_153_224

Perfect score: 369 Sequence: 1 KEKTPPEPKKEEVTIKANLIV.....GKYTVDAVKGYTLNIKFAQ 72

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Number DB seq length: 0 Number DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_23;*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_rodent:*
- 13: sp_vertebrate:*
- 14: sp_virus:*
- 15: sp_unclassified:*
- 16: sp_rvirus:*
- 17: sp_bacteriap:*
- 17: sp_archeap:*

SPTREMBL_23;*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_rodent:*

13: sp_vertebrate:*

14: sp_virus:*

15: sp_unclassified:*

16: sp_rvirus:*

17: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	369	100.0	455	2	053291		Q53291 streptococc
2	369	100.0	719	2	051912		Q51912 peptostrept
3	315	85.4	992	2	051918		Q51918 peptostrept
4	88.5	24.0	216	4	09BPV7		Q9BPV7 homo sapien
5	88.5	24.0	398	4	Q9BPZ1		Q9BPZ1 homo sapien
6	83.5	22.6	398	11	Q9CZ02		Q9CZ02 mus musculus
7	83.5	22.6	398	11	Q91WD1		Q91WD1 mus musculus
8	82.5	22.4	1576	16	Q9ZEV8		Q9ZEV8 yersinia pe
9	74	20.1	871	10	Q9LMB2		Q9LMB2 arabidopsis
10	73.5	19.9	256	5	Q27039		Q27039 theiliera p
11	73.5	19.9	256	5	Q27039		Q27039 theiliera p
12	73.5	19.9	280	5	Q27030		Q27030 theiliera p
13	72	19.5	1025	10	Q9JME3		Q9JME3 arabidopsis
14	71	19.2	265	10	Q23822		Q23822 dunalieilla
15	69	18.7	324	3	Q9UUK3		Q9UUK3 schizosaccharomyces pombe
16	68	18.4	448	10	Q9SKP0		Q9SKP0 arabidopsis

ALIGNMENTS

RESULT 1

ID	Q53291	PRELIMINARY;	PRT;	455 AA.
AC	Q53291;			
DT	01-NOV-1996 (TREMBLrel.	01,	Created)	
DT	01-NOV-1996 (TREMBLrel.	01,	Last sequence update)	
DT	01-DEC-2001 (TREMBLrel.	19,	Last annotation update)	
DE	Protein LG (Fragment).			
OS	Streptococcus sp.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus			
OX	NCBI_TAXID=1106;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93094283; PubMed-1460053;			
RA	Kihlberg B.M., Sjöbring U., Kastren W., Björck L.;			
RT	"Protein LG: a hybrid molecule with unique immunoglobulin binding properties."			
RT	Properties."			
RL	J. Biol. Chem. 267:25583-25588(1992).			
DR	EMBL: SS0809; AAA03280.1; -;			
DR	HSSP; P06654; 1PGX;			
DR	InterPro; IPR03147; B1.			
DR	InterPro; IPR00724; IgG_bind_B.			
DR	Pfam; PF02246; B1; 4			
PT	NON_TER 455			
PT	SEQUENCE 455 AA: 49926 MW;			
DR	381FC235BBC8307B CRC64;			

Query Match 100.0%; Score 369; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2, 4e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 KETKPEEPKEEVTIKANLIVADGKTQAEFKGTFFEAAYRADLJAKENKYTVDA 60

Db 174 KETKPEEPKEEVTIKANLIVADGKTQAEFKGTFFEAAYRADLJAKENKYTVDA 233

Qy 61 DKGYTLNIKFLAG 72

Db 234 DKGYTLNIKFLAG 245

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278B-1_COPY_153_224

Perfect score: 369

Sequence: 1 KERKPEEPKEEVTKANLIY.....GKTTVDVADRGYTNIKFAG 72

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

ched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0‡ Maximum Match 100‡ Listing First 45 summaries

Database : PIR 76.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	455	A45063	immunoglobulin-binding protein LG - Peptostreptococcus magnus
2	369	100.0	455	A42808	Ig light chain-bin
3	315	85.4	992	S54396	protein L precursor
4	162	43.9	74	A34483	Ig light chain-bin
5	82.5	22.4	1576	AB0249	probable hemolysin
6	80.5	21.8	395	A43700	BN51 protein - hum
7	74	20.1	871	D86355	merocrine surface
8	73.5	19.9	256	S54803	hypothetical prote
9	72	19.5	1025	E86355	late embryogenesis
10	69	18.7	324	T37931	leukotoxin A - Pas
11	68	18.4	448	H84782	probable cell surf
12	67	18.2	2	B30169	late embryogenesis
13	66.5	18.0	657	AD1525	PAD dependent oxid
14	66	17.9	448	JC6171	glycolate oxidase
15	66	17.9	470	AF2828	hypothetical prote
16	66	17.9	477	D97606	tryptophanase (EC
17	65.5	17.8	436	T16638	tryptophanase (imp
18	65.5	17.8	448	W2BC	DNA-directed DNA p
19	65.5	17.8	476	E91209	RTX toxin RTx VC1
20	65.5	17.8	476	H86055	methyl-accepting c
21	65.5	17.8	1179	T35093	hypothetical prote
22	65.5	17.8	4558	C82199	hypothetical prote
23	65	17.6	636	H70184	nuclear lamin C pr
24	65	17.6	838	D71492	hypothetical prote
25	64.5	17.5	243	F72719	potassium channel
26	64	17.3	621	S49020	inward rectifier p
27	64	17.3	722	T21521	hypothetical prote
28	63.5	17.2	414	S48738	hypothetical prote
29	63.5	17.2	425	S52852	hypothetical prote

ALIGNMENTS

RESULT 1
A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus
C;Species: Peptostreptococcus magnus
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C;Accession: A45063
R;Kihlberg, B.M.; Sjöbring, U.; Kastern, W.; Björck, L.
J. Biol. Chem. 267, 25583-25586, 1992
A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties
A;Reference number: A45063; MUID:93094283; PMID:1450053
A;Accession: A45063
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Cross references: GB:S50099; NID:9261705; PID:AAA003280; 1; PID:G261706
A;Note: sequence extracted from NCBI backbone (NCBN:128302; NCBIPI:120303)

Query Match 100.0%; Score 369; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 6.8e-31;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KBKTPERPEKEVTIKANLIYADGKTTAEOFKGTFEEATAEAYRDYLAKENGKYTVDA 60
Db 174 KBKTPERPEKEVTIKANLIYADGKTTAEOFKGTFEEATAEAYRDYLAKENGKYTVDA 233

QY 61 DKGYTLNPKFAG 22
Db 234 DKGYTLNPKFAG 245

RESULT 2
A42808 Ig light chain-binding protein precursor - Peptostreptococcus magnus
C;Species: Peptostreptococcus magnus
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: A42808; A41493
R;Kastern, W.; Sjöbring, U.; Björck, L.
J. Biol. Chem. 267, 12820-12825, 1992
A;Title: Structure of Peptostreptococcal protein L and identification of a repeated
A;Reference number: A42808; MUID:923116971; PMID:16118782
A;Status: preliminary
A;Molecule type: DNA
A;Cross references: 1-719 <KAS>; GB:M86697
R;Kastern, W.; Holst, B.; Nielsen, E.; Sjöbring, U.; Björck, L.
Infect. Immun. 58, 1217-1222, 1990
A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence
A;Reference number: A41493; MUID:90215984; PMID:2108927
A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 202-275 <KA2>
 C;Keywords: immunoglobulin

Query Match 100.0%; Score 369; DB 2; Length 719;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTKANLYADGKTQTAEPKGTFEATAEYRADLAKENGKTYDVA 60
 Db 246 KEKTPPEPKKEVTKANLYADGKTQTAEPKGTFEATAEYRADLAKENGKTYDVA 305

Qy 61 DGYTNIKFG 72
 Db 306 DGYTNIKFG 317

RESULT 3

396 Protein L precursor - Peptostreptococcus magnus (strain 3316)

Species: Peptostreptococcus magnus
 Variety: strain 3316
 C;Date: 27-Oct-1996 #Sequence_revision 13-Mar-1997 #text_change 15-Oct-1999
 C;Accession: S54396
 P;Murphy, J. P.; Duggibley, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.R.
 Mol. Microbiol. 12, 911-920, 1994
 A;Title: The functional units of a peptotribofocal protein L.
 A;Reference number: S544396; MUID:95020613; PMID:7934898
 A;Accession: S54396
 A;Status: Preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-992 <MRB>
 A;Cross-references: EMBL:LO4466; NID:9150673; PIDN:AAA67503.1; PID:gi150674

Query Match 85.4%; Score 315; DB 2; Length 992;
 Best Local Similarity 85.7%; Pred. No. 7.1e-25;
 Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KTEPEPKKEVTKANLYADGKTQTAEPKGTFEATAEYRADLAKENGKTYDVA 62
 Db 468 ETPEPEPKKEVTKVNLLPADGKTQTAEPKGTFEATAEYRADLAKENGKTYDVA 527

Qy 63 GYTNIKFG 72
 Db 528 GYTNIKFG 537

RESULT 4

483 Ig light chain-binding protein L - Peptostreptococcus magnus (fragments)

Species: Peptostreptococcus magnus
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Aug-1996
 C;Accession: A34483
 R;Akerstrom, B.; Bjoerck, L.
 J. Biol. Chem. 264, 19740-19746, 1989
 A;Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz
 A;Accession: A34483
 A;Molecule type: Protein
 A;Residues: 1-74 <AKE>
 C;Keywords: immunoglobulin

Query Match 43.9%; Score 162; DB 2; Length 74;
 Best Local Similarity 62.5%; Pred. No. 4e-10;
 Matches 35; Conservative 3; Mismatches 2; Indels 16; Gaps 1;

Qy 2 EKTPPEPKKEVTKANLYADGKTQTAEPKG-----TPEEATAEA 41
 Db 9 EKTPPEPKKEVTKANLYADGKTQTAEPKG-----TPEEATAEA 64

RESULT 5

161 protein T16B15.12 [Imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #Sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C;Accession: AB0249
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, J.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Rutherford, K.; Simmonds, M.; Skilton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, J.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Rutherford, K.; Simmonds, M.; Skilton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001;
 A;Accession: AB0249
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1576 <KUR>
 A;Cross-references: GB:AU590842; PIDN:CAC90857.1; PID:gi15980056; GSPDB:GN00175
 C;Genetics:
 A;Gene: YPO2045

Query Match 22.4%; Score 82.5; DB 2; Length 1576;
 Best Local Similarity 27.5%; Pred. No. 2.4e-04;
 Matches 30; Conservative 9; Mismatches 27; Indels 43; Gaps 4;

Qy 1 KEKTPPEPKKEVTKANLYADGKTQTAEPKGTF-----EE----- 36
 Db 1001 KANTEQEKEVSRLG-----GNTATQEIKGHUVKAEFTSQGDGSYAEMLVGNINAKSG 1054

Qy 37 ---ATAEAYRADLAKENGKTYDVA-----VADKGYTNIKFG 72
 Db 1055 VSIKTTGDAYYYATNIEGGNGDITIDAGNNLYFFQDVQDSQRSSNIKFSG 1103

RESULT 6

443700 Protein - human

C;Species: Homo sapiens (man)
 C;Date: 03-Mar-1993 #Sequence_revision 03-Mar-1993 #text_change 21-Jul-2000
 C;Accession: A43700
 R;Ittman, M.; Greco, A.; Basilio, C.
 Mol. Cell. Biol. 7, 3386-3393, 1987
 A;Title: Isolation of the human gene that complements a temperature-sensitive cell
 A;Reference number: A43700; MUID:98065472; PMID:36833386
 A;Accession: A43700
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-95 <ITT>
 A;Cross-references: GB:MI7754; NID:gi179512; PIDN:AAAS1838.1; PID:gi179513
 C;Genetics:
 A;Gene: GDB:BN51T
 A;Cross-references: GDB:119728; OMIM:187280
 A;Map position: 8pter-8q24

Query Match 21.0%; Score 80.5; DB 2; Length 395;
 Best Local Similarity 32.1%; Pred. No. 0.84e-04;
 Matches 26; Conservative 9; Mismatches 27; Indels 19; Gaps 3;

Qy 3 KTEPEPKKEVTKANLYADGKTQTAEPKGTFEATAEYRADLAK 50
 Db 63 KTEPEPKKEVTKANLYADGKTQTAEPKGTFEATAEYRADLAK 50

Qy 51 ENGKYTVDADKG--YTLNIK 69
 Db 118 GNRDKTVDSMDGPShINIK 138

RESULT 7

D83355 protein T16B15.12 [Imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #Sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: D86155
 R;Theologis, A.J.; Becker, J.R.; Palm, C.J.; Feder Spiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewa, anaen, N.P.; Hughes, B.; Huidar, L.

RESULT 5

~249

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds
Perfect score: 370 (without alignments)
Sequence: 1 KERTPEEPKEEVTIKANLIV.....GKYTADLEDDGGYTINIRFAG 72

Title: US-08-325-278B-1_COPY_225_296

Scoring table: BLOSUM62
Gapop 10.0 , Gpext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_23:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_evirus:
 16: sp_bacteriaph:
 17: sp_archeap:
 18: sp_bacteriophage:
 19: sp_prokaryote:
 20: sp_eukaryote:
 21: sp_eukaryotic_cell:
 22: sp_eukaryotic_virus:
 23: sp_eukaryotic_nucleic_acid:
 24: sp_eukaryotic_protein:
 25: sp_eukaryotic_nucleic_acid:
 26: sp_eukaryotic_protein:
 27: sp_eukaryotic_nucleic_acid:
 28: sp_eukaryotic_protein:
 29: sp_eukaryotic_nucleic_acid:
 30: sp_eukaryotic_protein:
 31: sp_eukaryotic_nucleic_acid:
 32: sp_eukaryotic_protein:
 33: sp_eukaryotic_nucleic_acid:
 34: sp_eukaryotic_protein:
 35: sp_eukaryotic_nucleic_acid:
 36: sp_eukaryotic_protein:
 37: sp_eukaryotic_nucleic_acid:
 38: sp_eukaryotic_protein:
 39: sp_eukaryotic_nucleic_acid:
 40: sp_eukaryotic_protein:
 41: sp_eukaryotic_nucleic_acid:
 42: sp_eukaryotic_protein:
 43: sp_eukaryotic_nucleic_acid:
 44: sp_eukaryotic_protein:
 45: sp_eukaryotic_nucleic_acid:

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	370	100.0	455	2	Q53291	053291 streptococc	
2	370	100.0	719	2	Q51918	Q51912 peptostrept	
3	329	88.9	992	2	Q8ZEV8	Q8ZEV8 yersinia pe	
4	80.5	21.8	1576	16	Q9UUK3	Q9UUK3 schizosacch	
5	74	20.0	324	3	Q8RPV1	Q8RPV1 streptococc	
6	74	20.0	846	2	Q9BPV7	Q9BPV7 homo sapien	
7	71.5	19.3	216	4	Q9BPZ1	Q9BPZ1 homo sapien	
8	71.5	19.3	398	4	Q9BPZ1	Q9BPZ1 homo sapien	
9	71.5	19.3	657	2	Q9DS2	Q9DS2 listeria in	
10	71	19.2	871	10	Q9IME2	Q9IME2 arabidopsis	
11	70.5	19.1	256	5	Q27039	Q27039 thelleria p	
12	70.5	19.1	256	5	Q27029	Q27029 thelleria p	
13	70.5	19.1	280	5	Q27030	Q27030 thelleria p	
14	70.5	19.1	398	11	Q9CZ02	Q9CZ02 mus musculu	
15	70.5	19.1	398	11	Q9IWD1	Q9IWD1 mus musculu	
16	70	18.9	549	17	Q8TZL6	Q8TZL6 pyrococcus	

ALIGNMENTS

RESULT 1	Q53291	SEQUENCE FROM N.A. ID Q53291 PRELIMINARY;	PRT; 455 AA.
	AC Q53291;	AC Q53291; (TREMBLrel.	
	DT 01-NOV-1996	DT 01-NOV-1996 (TREMBLrel.	01, Created)
	DT 01-DEC-2001	DT 01-DEC-2001 (TREMBLrel.	01, Last sequence update)
	DT Protein LG (Fragment).	DT Protein LG (Fragment).	
	DE Streptococcus sp.	OS Streptococcus sp.	
	OC Bacteria; Firmicutes;	OC Bacteria; Firmicutes; Streptococcaceae;	
	OC Streptococcus	OX NCBL_TAXID=1306;	
	OX [1]	RN [1]	
	RP SEQUENCE FROM N.A. MEDLINE=91094383; PubMed=1460053;	RX Kihlberg B.M., Sjöbring U., Kastern W., Björck L..	
	DR "Protein LG: a hybrid molecule with unique immunoglobulin binding properties."	RA "Protein LG: a hybrid molecule with unique immunoglobulin binding properties."	
	RT PROTEIN LG (Fragment).	RT PROTEIN LG (Fragment).	
	RL J. Biol. Chem. 267:25583-25588(1992).	RL EMBL: S50809; AAA03280..; -	
	DR HSSP; P06654; IPGX.	DR InterPro; IPR00147; B1.	
	DR InterPro; IPR000724; IgG_bind_B.	DR PF0246; B1; 4.	
	DR PFam; PF01378; IgG_binding-B; 2.	DR FT NON_TER 455 AA; 49926 MN; 38LFC235BBC8307B CRC64	
	SO	FT NON_TER 455 AA; 49926 MN; 38LFC235BBC8307B CRC64	
	Query Match Score 370; DB 2; Length 455;	Best Local Similarity 100.0%; Pred. No. 6.5e-30;	
	Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	370	100.0	455	2	Q53291	053291 streptococc	
2	370	100.0	719	2	Q51912	Q51912 peptostrept	
3	329	88.9	992	2	Q8ZEV8	Q8ZEV8 yersinia pe	
4	80.5	21.8	1576	16	Q9UUK3	Q9UUK3 schizosacch	
5	74	20.0	324	3	Q8RPV1	Q8RPV1 streptococc	
6	74	20.0	846	2	Q9BPV7	Q9BPV7 homo sapien	
7	71.5	19.3	216	4	Q9BPZ1	Q9BPZ1 homo sapien	
8	71.5	19.3	398	4	Q9BPZ1	Q9BPZ1 homo sapien	
9	71.5	19.3	657	2	Q9DS2	Q9DS2 listeria in	
10	71	19.2	871	10	Q9IME2	Q9IME2 arabidopsis	
11	70.5	19.1	256	5	Q27039	Q27039 thelleria p	
12	70.5	19.1	256	5	Q27029	Q27029 thelleria p	
13	70.5	19.1	280	5	Q27030	Q27030 thelleria p	
14	70.5	19.1	398	11	Q9CZ02	Q9CZ02 mus musculu	
15	70.5	19.1	398	11	Q9IWD1	Q9IWD1 mus musculu	
16	70	18.9	549	17	Q8TZL6	Q8TZL6 pyrococcus	

RESULT 2								
Q51912		SEQUENCE FROM N.A.						
TD	051912; PRELIMINARY;	PRT;	719 AA.					
AC	Q51912; 1996 (TREMBLrel. 01, Created)							
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)							
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)							
DE	Protein L precursor.							
OS	Peptostreptococcus magnus.							
OC	Bacteria; Firmicutes; Clostridia; Clostridiales;							
OX	Peptostreptocaceae; Finegoldia.							
RB	NCBI_TAXID=1260;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=312;							
RX	MEDLINE=95018460; PubMed=7987012;							
RA	Murphy J.P., Trovern A.R., Duggal, Eby C.J.;							
RT	"Nucleotide sequence of the gene for peptostreptococcal protein L."							
RL	-1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY AN AMIDE BOND (BY SIMILARITY).							
CC	HSSP: Q51911; AAA67503.1;							
DR	EMBL: L04466; AAA67503.1;							
DR	DR InterPro: IPRO03147; BL1.							
DR	InterPro: IPRO02988; GA.							
DR	InterPro: IPRO01899; Gram_pos_anchor.							
DR	InterPro: IPRO06192; LPXTG.							
PFam	PF01246; B1; 4.							
PFam	PF01468; GA; 4.							
DR	TIGRFAMS; TIGR01167; LPXTG_anchor; 1.							
DR	PROSITE; PS50847; GRAM_POS_ANCHORING; 1.							
KW	Cell wall; Peptidoglycan_anchor; Signal.							
FT	SIGNAL 1 24 POTENTIAL.							
FT	CHAIN 25 992 PROTEIN L.							
SQ	SEQUENCE 992 AA; 108700 MW; 9CFF77157845DCE CRC64;							
Query Match Score 88.9%; Best Local Similarity 80.0%; DR 2; Length 992; Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;								
Qy 3 KTPPEPKKEEVTIKANLYIADGKTTAEGKTFEAATAEAYRADLAKNGKYTADELGD 62 Db 468 ETPEPEKEEVTIKVNLFADGKTTAEGKTFEAATAEAYRADLAKNGYETADLEDG 527								
Qy 63 GYTINPRFAG 72 Db 528 GYTINIKFAG 537								
RESULT 4								
Q8ZEV8 PRELIMINARY; PRT; 1576 AA.								
ID	Q8ZEV8							
AC	Q8ZEV8;							
DT	01-MAR-2002 (TREMBLrel. 20, Created)							
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)							
DB	01-MAR-2003 (TREMBLrel. 23, Last annotation update)							
DE	Putative hemolysin.							
GN	YPO2045 OR Y2267.							
OS	Yersinia pestis.							
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; NCBI_TaxID=632;							
RN	[1]							
SEQUENCE FROM N.A.								
RC	STRAIN=CO-92 / Biovar Orientalis; MEDLINE=2147043; PubMed=11586360;							
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Brooks S., Basham D., Bentley S.D., Davies R.M., Cerdeiro-Tarraga A.M., Chillingworth T., Cronin A., Davies P., Duran P., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; RT "Genome sequence of Yersinia pestis, the causative agent of plague.";							
RN	[2]							
SEQUENCE FROM N.A.								
RC	STRAIN=KIM5 / Biovar Mediaevalis; MEDLINE=22137863; PubMed=2142430;							
RA	Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D., RT "Genome sequence of Yersinia pestis KIM5."							
RN	[2]							

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds
(without alignments)
406.975 Million cell updates/sec

Title: US-08-325-278B-1_COPY_225_296

Perfect score: 370

Sequence: 1 KEKTPPEEKVTKANLIV.....GKYTALEDDGGYTINIRFAG 72

Scoring table: BLOSUM62

GapPen 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Maximum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	370	100.0	455	2	A45063	immunoglobulin-binding protein LG - Peptostreptococcus magnus
2	370	100.0	719	2	A42808	C;Species: Peptostreptococcus magnus
3	329	88.9	992	2	S54396	C;Accession: A45063
4	157	42.4	74	2	A34483	R;Kihlberg, B.M.; Sjobring, U.; Kastern, W.; Björck, L. J. Biol. Chem. 267: 25533-25588, 1992
5	80.5	21.8	1576	2	AE0249	A;Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties
6	71.74	20.0	324	2	T37931	A;Reference number: A45063; PMID:1460053
7	71.5	19.3	657	2	AD1525	A;Status: Preliminary
8	70.5	19.1	256	2	D86355	A;Molecule type: mRNA; protein
9	71	19.2	871	2	S54803	A;Residues: 1-455 <KH>
10	69	18.8	2062	2	G96602	A;Cross-references: GB:S50809; NID:9261705; PIDN:AAA03280_1; PID:9261706; NCBI:120302; NCBI:120303
11	69	18.6	397	2	AC1498	A;Note: sequence extracted from NCBI Backbone (NCBIN:120302, NCBI:120303)
12	69	18.6	401	2	AE1498	Query Match 100.0%; Score 370; DB 2; Length 455; Best Local Similarity 100.0%; Pred. No. 4.3e-32; Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13	69	18.6	1025	2	E86355	Qy 1 KEKTPPEEKVTKANLIVADGKQTAEFKGTAEEYRADLLAKENKYTADEL 60 Db 246 KEKTPPEEKVTKANLIVADGKQTAEFKGTAEEYRADLLAKENKYTADEL 305
14	68.5	18.5	858	2	E96602	Qy 61 DGGYTINIRFAG 72 Db 306 DGGYTINIRFAG 317
15	67	18.1	283	2	S69639	RESULT 2
16	66.5	18.0	1029	2	F96602	A42808 Ig light chain-binding protein precursor - Peptostreptococcus magnus N;Alternative names: Protein L C;Species: Peptostreptococcus magnus
17	66	17.8	495	2	D89803	C;Date: 19-May-1994 #sequence_revision 19-May-1994 R;Kastern, W.; Sjoerbring, U.; Björck, L. J. Biol. Chem. 267: 12820-12825, 1992
18	65.5	17.7	4558	2	C82199	A;Title: Structure of peptostreptococcal protein L and identification of a repeated
19	64	17.4	1179	2	T35053	A;Reference number: A42808; PMID:92316971; PMID:1618782
20	64	17.3	863	2	S06017	A;Status: preliminary
21	64	17.3	2364	2	A56577	A;Molecule type: DNA A;Accession: A42808 A;Residues: 1-719 <KAS>
22	64	17.3	2464	1	QRMSP1	A;Cross-references: GB:M86637 R;Kastern, W.; Holst, E.; Nielsen, E.; Sjoerbring, U.; Björck, L. Infect. Immun. 58, 1217-1222, 1990
23	63.5	17.2	395	2	A43700	A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence factor
24	63.5	17.2	550	2	F75186	A;Reference number: A41493; PMID:90215984; PMID:2108927 A;Accession: A41493
25	63	17.0	356	2	T37136	A;Status: preliminary
26	63	17.0	490	2	F38462	A;Cross-references: GB:M86637 R;Kastern, W.; Holst, E.; Nielsen, E.; Sjoerbring, U.; Björck, L. Infect. Immun. 58, 1217-1222, 1990
27	63	17.0	1104	1	A36866	A;Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence factor
28	62.5	16.9	215	2	AC1156	A;Reference number: A41493; PMID:90215984; PMID:2108927 A;Accession: A41493
29	62	16.8	266	2	AI2289	A;Status: preliminary

probable hemolysin YPO2045 [imported] - <i>Yersinia pestis</i> (strain C092)											
C:Species: <i>Yersinia pestis</i>											
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001											
C:Accession: AE0249											
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentit, A.; Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature, 413, 523-527, 2001											
A:Title: Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague.											
A:Reference number: AB0001; MUID:21470413; PMID:11586360											
A:Accession: AE0249											
A:Status: preliminary											
A:Molecule type: DNA											
A:Cross references: GB:AL590842; PIDN:CAC90857.1; PID:g15980056; GSPDB:GN00175											
C:Genetics:											
A:Gene: YPO2045											
S:UNIT 3											
Query Match Score 370; DB 2; Length 719;											
Best Local Similarity 100.0%; Pred. No. 7.2e-32; Indels 0; Gaps 0;											
Mismatches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
C:Residues: 61 DGYYTINIRFAG 72											
378 DGYYTINIRFAG 389											
S:UNIT 3											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 3											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 6											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 6											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											
S:UNIT 7											
Query Match Score 21.8%; Score 80.5%; DB 2; Length 1576;											
Best Local Similarity 25.7%; Pred. No. 2.6%;											
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;											
C:Residues: 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 60											
318 KEKTPPEPKKEVTIKANLIYADGKTQTAEEFKGTFAATAEAYRDAYDLAKENGKYTADLE 377											